SEQUENCE LISTING

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<120> PLANT MSH2 SEQUENCES AND METHODS OF USE

<130> 5839-2 (035839/196219)

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<170> PatentIn version 3.0

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Phe Phe Lys Thr Leu Pro Lys Asp Pro Arg Ala Val Arg Leu Phe Asp
            30                  35                  40

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Arg Arg Asp Tyr Tyr Thr Ser His Gly Asp Asp Ala Thr Phe Ile Ala
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Glu Thr Tyr Tyr His Thr Thr Thr Ala Leu Arg Gln Leu Gly Asn Arg
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Ile Ala Arg Asp Ile Leu Leu Glu Arg Met Asp Arg Thr Leu Glu Leu
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ggg aat ctt gga agt ttt gag gat att ctg ttt gct aat aat gaa atg
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Gly Asn Leu Gly Ser Phe Glu Asp Ile Leu Phe Ala Asn Asn Glu Met
125 130 135

caa aat tct ccg gtg att gct gct ctt gct cca aac ttc ggt cag aat
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Gln Asn Ser Pro Val Ile Ala Ala Leu Ala Pro Asn Phe Gly Gln Asn
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Gly Cys Glu Val Gly Leu Gly Tyr Val Asp Ile Thr Lys Arg Val Leu
155 160 165 170

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579
Gly Leu Thr Glu Phe Leu Asp Asp Ser His Phe Thr Asn Leu Glu Ser
175 180 185

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627
Ala Leu Val Ala Leu Gly Cys Arg Glu Cys Leu Val Pro Ala Glu Thr
190 195 200

ggc aaa tcc agt gaa tac agg cct atg ttt gat gca ata tct aga tgc
675
Gly Lys Ser Ser Glu Tyr Arg Pro Met Phe Asp Ala Ile Ser Arg Cys
205 210 215

ggc gtg atg gta act gaa aga aag aaa act gaa ttt aaa ggg aga gat
723
Gly Val Met Val Thr Glu Arg Lys Lys Thr Glu Phe Lys Gly Arg Asp
220 225 230

ttg gta cag gat ctt ggt agg ctc gtc aag ggt tca gta gaa cct gtt
771
Leu Val Gln Asp Leu Gly Arg Leu Val Lys Gly Ser Val Glu Pro Val
235 240 245 250

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819
Arg Asp Leu Val Ser Gly Phe Glu Cys Ala Ser Gly Ala Leu Gly Cys
255 260 265

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867
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270 275 280

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915

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Tyr Thr Val Lys Gln Tyr Asn Leu Asn Ser Tyr Met Arg Leu Asp Ser
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gct gct atg aga gca ctg aat gtt atg gag agc aaa tca gat gct aat
963
Ala Ala Met Arg Ala Leu Asn Val Met Glu Ser Lys Ser Asp Ala Asn
    300                 305                 310

aaa aat ttt agc ttg ttc ggt ctg atg aat aga acg tgt act gct gga
1011
Lys Asn Phe Ser Leu Phe Gly Leu Met Asn Arg Thr Cys Thr Ala Gly
315                 320                 325                 330

atg ggt aaa agg tta ttg cac atg tgg ctg aag caa cct tta cta gat
1059
Met Gly Lys Arg Leu Leu His Met Trp Leu Lys Gln Pro Leu Leu Asp
                335                 340                 345

gta gaa gag att aac tgt agg ctg gat tta gtt caa tca ttc gtg gag
1107
Val Glu Glu Ile Asn Cys Arg Leu Asp Leu Val Gln Ser Phe Val Glu
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gat gct gcg ctt cgc caa gat ttg agg cag cat ctg aaa aga att tca
1155
Asp Ala Ala Leu Arg Gln Asp Leu Arg Gln His Leu Lys Arg Ile Ser
        365                 370                 375

gat att gag cgg ctg aca cac aat ctt gag agg aaa aga gcc agt tta
1203
Asp Ile Glu Arg Leu Thr His Asn Leu Glu Arg Lys Arg Ala Ser Leu
    380                 385                 390

gtg cac gtt gta aaa ctc tat cag tca agt acc aga gta cca tat atc
1251
Val His Val Val Lys Leu Tyr Gln Ser Ser Thr Arg Val Pro Tyr Ile
395                 400                 405                 410

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1299
Lys Ser Val Leu Glu Arg His Asp Gly Gln Phe Ala Thr Leu Ile Arg
                415                 420                 425

gaa agg tat att gat tct cta gag aaa tgg agt gat gat aat cac ctg
1347
Glu Arg Tyr Ile Asp Ser Leu Glu Lys Trp Ser Asp Asp Asn His Leu
            430                 435                 440

aat aag ttc ata ggt ctt gtg gaa act tct gtt gac ctt gat caa ctt
1395
Asn Lys Phe Ile Gly Leu Val Glu Thr Ser Val Asp Leu Asp Gln Leu
        445                 450                 455

gag aat gga gaa tac atg att tct tct gca tat gac cca aat tta tct
1443
Glu Asn Gly Glu Tyr Met Ile Ser Ser Ala Tyr Asp Pro Asn Leu Ser
    460                 465                 470

gct ctg aag gat gag caa gag aca ttg gag cga caa att cat aat ttg
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1491
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cac aaa caa act gcc aat gat ctt gat cta cct att gat aag tca ctt
1539
His Lys Gln Thr Ala Asn Asp Leu Asp Leu Pro Ile Asp Lys Ser Leu
                495                 500                 505

aaa cta gat aaa gaa aca caa ttt gga cac gtc ttc aga att acc aag
1587
Lys Leu Asp Lys Glu Thr Gln Phe Gly His Val Phe Arg Ile Thr Lys
            510                 515                 520

aaa gaa gaa cca aaa gtc agg aag cag cta aat tct cac tac att gtt
1635
Lys Glu Glu Pro Lys Val Arg Lys Gln Leu Asn Ser His Tyr Ile Val
        525                 530                 535

ctc gaa aca cgt aag gat ggg gta aag ttc acc tat aca aaa ctc aaa
1683
Leu Glu Thr Arg Lys Asp Gly Val Lys Phe Thr Tyr Thr Lys Leu Lys
    540                 545                 550

aaa cta gga gat cag ttc cag aag att gta gag gag tac aaa agc tgt
1731
Lys Leu Gly Asp Gln Phe Gln Lys Ile Val Glu Glu Tyr Lys Ser Cys
555                 560                 565                 570

cag aaa gaa ttg gta gct cgt gta gtt caa aca gct gcg agt ttc tcc
1779
Gln Lys Glu Leu Val Ala Arg Val Val Gln Thr Ala Ala Ser Phe Ser
                575                 580                 585

gag gtg ttt gca ggt ata gct ggt gta ctt gct gag ttg gat gtg tta
1827
Glu Val Phe Ala Gly Ile Ala Gly Val Leu Ala Glu Leu Asp Val Leu
            590                 595                 600

ctg agt ttt gcg gat ttg gct gcc agt tgc cca act ccc tac aca aga
1875
Leu Ser Phe Ala Asp Leu Ala Ala Ser Cys Pro Thr Pro Tyr Thr Arg
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cca aat atc agt cca cca gat aca gga gat att ata ctt gaa ggg tgt
1923
Pro Asn Ile Ser Pro Pro Asp Thr Gly Asp Ile Ile Leu Glu Gly Cys
    620                 625                 630

agg cat cct tgt gtg gaa gct caa gat tgg gtt aac tcc att cct aat
1971
Arg His Pro Cys Val Glu Ala Gln Asp Trp Val Asn Ser Ile Pro Asn
635                 640                 645                 650

gac tgt aga cta gtt agg gga gag agt tgg ttt cag att atc aca ggc
2019
Asp Cys Arg Leu Val Arg Gly Glu Ser Trp Phe Gln Ile Ile Thr Gly
                655                 660                 665
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2067
Pro Asn Met Gly Gly Lys Ser Thr Tyr Ile Arg Gln Val Gly Val Asn
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gtc ctg atg gcc caa gtt ggc tcg ttt gtt cca tgt gac aat gct acc
2115
Val Leu Met Ala Gln Val Gly Ser Phe Val Pro Cys Asp Asn Ala Thr
        685                 690                 695

att tct att cgt gat tgt att ttt gct cgt gtt ggc gct gga gat tgc
2163
Ile Ser Ile Arg Asp Cys Ile Phe Ala Arg Val Gly Ala Gly Asp Cys
    700                 705                 710

cag ctg aga gga gtt tct act ttt atg caa gag atg ctt gag act gca
2211
Gln Leu Arg Gly Val Ser Thr Phe Met Gln Glu Met Leu Glu Thr Ala
715                 720                 725                 730

tcg atc ttg aaa gga gct act gat aga tca ttg att ata att gat gag
2259
Ser Ile Leu Lys Gly Ala Thr Asp Arg Ser Leu Ile Ile Ile Asp Glu
                735                 740                 745

ttg ggc cgt ggg aca tca acc tac gat ggc ttt ggt tta gct tgg gct
2307
Leu Gly Arg Gly Thr Ser Thr Tyr Asp Gly Phe Gly Leu Ala Trp Ala
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2355
Ile Cys Glu His Ile Val Glu Glu Ile Lys Ala Pro Thr Leu Phe Ala
        765                 770                 775

act cac ttt cat gag ctg act gca tta gcc aac aag aat gga gac aat
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Thr His Phe His Glu Leu Thr Ala Leu Ala Asn Lys Asn Gly Asp Asn
    780                 785                 790

gga cat aag aaa aat gct ggg ata gca aat ttt cat gtt ttt gca cac
2451
Gly His Lys Lys Asn Ala Gly Ile Ala Asn Phe His Val Phe Ala His
795                 800                 805                 810

att gac cct tct aat cgc aag cta act atg ctt tac aag gtt cac cca
2499
Ile Asp Pro Ser Asn Arg Lys Leu Thr Met Leu Tyr Lys Val His Pro
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ggt gct tgt gat cag agt ttt ggt att cat gtt gct gaa ttt gca aat
2547
Gly Ala Cys Asp Gln Ser Phe Gly Ile His Val Ala Glu Phe Ala Asn
            830                 835                 840

ttt cca ccg agt gtt gtg gct ctg gct aga gaa aag gca tct gag ttg
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Phe Pro Pro Ser Val Val Ala Leu Ala Arg Glu Lys Ala Ser Glu Leu
        845                 850                 855
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gct tca aaa cgg aag aga gaa ttt gac cgc cat gac gtg tct aga ggt
2691
Ala Ser Lys Arg Lys Arg Glu Phe Asp Arg His Asp Val Ser Arg Gly
875 880 885 890

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2739
Thr Ala Arg Ala Arg Gln Phe Leu Gln Asp Phe Ala Gln Leu Pro Leu
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2787
Asp Lys Met Asp Pro Asn Val Val Arg Gln Lys Leu Ser Lys Met Lys
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acc gac ctg gag agg gat gca gtt gac tct cac tgg ctt cag caa ttc
2835
Thr Asp Leu Glu Arg Asp Ala Val Asp Ser His Trp Leu Gln Gln Phe
925 930 935

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Phe

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Lys Asp Pro Arg Ala Val Arg Leu Phe Asp Arg Arg Asp Tyr Tyr Thr
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Ser His Gly Asp Asp Ala Thr Phe Ile Ala Glu Thr Tyr Tyr His Thr
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Thr Thr Ala Leu Arg Gln Leu Gly Asn Arg Ala Asp Ala Leu Ser Ser
65                  70                  75                  80

Val Ser Val Ser Arg Asn Met Phe Glu Thr Ile Ala Arg Asp Ile Leu
                85                  90                  95

Leu Glu Arg Met Asp Arg Thr Leu Glu Leu Tyr Glu Gly Ser Gly Ser
            100                 105                 110

Asn Trp Arg Leu Val Lys Ser Gly Thr Pro Gly Asn Leu Gly Ser Phe
        115                 120                 125

Glu Asp Ile Leu Phe Ala Asn Asn Glu Met Gln Asn Ser Pro Val Ile
    130                 135                 140

Ala Ala Leu Ala Pro Asn Phe Gly Gln Asn Gly Cys Glu Val Gly Leu
145                 150                 155                 160

Gly Tyr Val Asp Ile Thr Lys Arg Val Leu Gly Leu Thr Glu Phe Leu
                165                 170                 175

Asp Asp Ser His Phe Thr Asn Leu Glu Ser Ala Leu Val Ala Leu Gly
            180                 185                 190

Cys Arg Glu Cys Leu Val Pro Ala Glu Thr Gly Lys Ser Ser Glu Tyr
        195                 200                 205

Arg Pro Met Phe Asp Ala Ile Ser Arg Cys Gly Val Met Val Thr Glu
    210                 215                 220

Arg Lys Lys Thr Glu Phe Lys Gly Arg Asp Leu Val Gln Asp Leu Gly
225                 230                 235                 240

Arg Leu Val Lys Gly Ser Val Glu Pro Val Arg Asp Leu Val Ser Gly
                245                 250                 255

Phe Glu Cys Ala Ser Gly Ala Leu Gly Cys Ile Leu Ser Tyr Ala Glu
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Leu Leu Ala Asp Glu Ser Asn Tyr Gly Asn Tyr Thr Val Lys Gln Tyr
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Asn Val Met Glu Ser Lys Ser Asp Ala Asn Lys Asn Phe Ser Leu Phe
305                 310                 315                 320

Gly Leu Met Asn Arg Thr Cys Thr Ala Gly Met Gly Lys Arg Leu Leu
                325                 330                 335

His Met Trp Leu Lys Gln Pro Leu Leu Asp Val Glu Glu Ile Asn Cys
            340                 345                 350

Arg Leu Asp Leu Val Gln Ser Phe Val Glu Asp Ala Ala Leu Arg Gln
        355                 360                 365

Asp Leu Arg Gln His Leu Lys Arg Ile Ser Asp Ile Glu Arg Leu Thr
    370                 375                 380

His Asn Leu Glu Arg Lys Arg Ala Ser Leu Val His Val Val Lys Leu
385                 390                 395                 400

Tyr Gln Ser Ser Thr Arg Val Pro Tyr Ile Lys Ser Val Leu Glu Arg
                405                 410                 415

His Asp Gly Gln Phe Ala Thr Leu Ile Arg Glu Arg Tyr Ile Asp Ser
            420                 425                 430

Leu Glu Lys Trp Ser Asp Asp Asn His Leu Asn Lys Phe Ile Gly Leu
        435                 440                 445

Val Glu Thr Ser Val Asp Leu Asp Gln Leu Glu Asn Gly Glu Tyr Met
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Ile Ser Ser Ala Tyr Asp Pro Asn Leu Ser Ala Leu Lys Asp Glu Gln
465                 470                 475                 480

Glu Thr Leu Glu Arg Gln Ile His Asn Leu His Lys Gln Thr Ala Asn
                485                 490                 495

Asp Leu Asp Leu Pro Ile Asp Lys Ser Leu Lys Leu Asp Lys Glu Thr
            500                 505                 510

Gln Phe Gly His Val Phe Arg Ile Thr Lys Lys Glu Glu Pro Lys Val
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515 520 525

Arg Lys Gln Leu Asn Ser His Tyr Ile Val Leu Glu Thr Arg Lys Asp
530 535 540

Gly Val Lys Phe Thr Tyr Thr Lys Leu Lys Lys Leu Gly Asp Gln Phe
545 550 555 560

Gln Lys Ile Val Glu Glu Tyr Lys Ser Cys Gln Lys Glu Leu Val Ala
565 570 575

Arg Val Val Gln Thr Ala Ala Ser Phe Ser Glu Val Phe Ala Gly Ile
580 585 590

Ala Gly Val Leu Ala Glu Leu Asp Val Leu Leu Ser Phe Ala Asp Leu
595 600 605

Ala Ala Ser Cys Pro Thr Pro Tyr Thr Arg Pro Asn Ile Ser Pro Pro
610 615 620

Asp Thr Gly Asp Ile Ile Leu Glu Gly Cys Arg His Pro Cys Val Glu
625 630 635 640

Ala Gln Asp Trp Val Asn Ser Ile Pro Asn Asp Cys Arg Leu Val Arg
645 650 655

Gly Glu Ser Trp Phe Gln Ile Ile Thr Gly Pro Asn Met Gly Gly Lys
660 665 670

Ser Thr Tyr Ile Arg Gln Val Gly Val Asn Val Leu Met Ala Gln Val
675 680 685

Gly Ser Phe Val Pro Cys Asp Asn Ala Thr Ile Ser Ile Arg Asp Cys
690 695 700

Ile Phe Ala Arg Val Gly Ala Gly Asp Cys Gln Leu Arg Gly Val Ser
705 710 715 720

Thr Phe Met Gln Glu Met Leu Glu Thr Ala Ser Ile Leu Lys Gly Ala
725 730 735

Thr Asp Arg Ser Leu Ile Ile Ile Asp Glu Leu Gly Arg Gly Thr Ser
740 745 750

Thr Tyr Asp Gly Phe Gly Leu Ala Trp Ala Ile Cys Glu His Ile Val
755 760 765

Glu Glu Ile Lys Ala Pro Thr Leu Phe Ala Thr His Phe His Glu Leu
770 775 780

Thr Ala Leu Ala Asn Lys Asn Gly Asp Asn Gly His Lys Lys Asn Ala
785 790 795 800

Gly Ile Ala Asn Phe His Val Phe Ala His Ile Asp Pro Ser Asn Arg
805 810 815

Lys Leu Thr Met Leu Tyr Lys Val His Pro Gly Ala Cys Asp Gln Ser
820 825 830

Phe Gly Ile His Val Ala Glu Phe Ala Asn Phe Pro Pro Ser Val Val
835 840 845

Ala Leu Ala Arg Glu Lys Ala Ser Glu Leu Glu Asp Phe Ser Pro Ile
850 855 860

Ala Ile Ile Pro Asn Asp Ile Lys Glu Ala Ala Ser Lys Arg Lys Arg
865 870 875 880

Glu Phe Asp Arg His Asp Val Ser Arg Gly Thr Ala Arg Ala Arg Gln
885 890 895

Phe Leu Gln Asp Phe Ala Gln Leu Pro Leu Asp Lys Met Asp Pro Asn
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915 920 925

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99
Leu Pro Glu Leu Lys Leu Asp Ala Lys Gln Ala Gln Gly Phe Leu Ser
                15                  20                  25

ttt ttc aaa acc cta ccc aag gac cct agg gca gtt cgc ctc ttt gat
147
Phe Phe Lys Thr Leu Pro Lys Asp Pro Arg Ala Val Arg Leu Phe Asp
            30                  35                  40

cgt cgg gac tat tat act gct cat gga gat gat gca act ttc att gca
195
Arg Arg Asp Tyr Tyr Thr Ala His Gly Asp Asp Ala Thr Phe Ile Ala
        45                  50                  55

gag aca tat tac cac aca aca act gcg tta cga cag ttg ggt aat aga
243
Glu Thr Tyr Tyr His Thr Thr Thr Ala Leu Arg Gln Leu Gly Asn Arg
    60                  65                  70

gct gat gcc ctt tcc agt gtt agt gtg agt aga aac atg ttt gaa aca
291
Ala Asp Ala Leu Ser Ser Val Ser Val Ser Arg Asn Met Phe Glu Thr
75                  80                  85                  90

ata gct cgt gac att ctc ttg gag aga atg gac cgt act ctt gaa cta
339
Ile Ala Arg Asp Ile Leu Leu Glu Arg Met Asp Arg Thr Leu Glu Leu
                95                  100                 105

tat gag ggc agt ggt tca aac tgg aga ctg gta aaa agt gga acc cca
387
Tyr Glu Gly Ser Gly Ser Asn Trp Arg Leu Val Lys Ser Gly Thr Pro
            110                 115                 120

ggg aat ctt gga agt ttt gag gat att ctg ttt gct aat aat gaa atg
435
Gly Asn Leu Gly Ser Phe Glu Asp Ile Leu Phe Ala Asn Asn Glu Met
        125                 130                 135

caa aat tct ccg gtg att gct gct ctt gct cca aac ttc ggt cag aat
483
Gln Asn Ser Pro Val Ile Ala Ala Leu Ala Pro Asn Phe Gly Gln Asn
    140                 145                 150

gga tgt gaa gtt ggc tta ggc tat gtt gat att act aag aga gtc ctt
531
Gly Cys Glu Val Gly Leu Gly Tyr Val Asp Ile Thr Lys Arg Val Leu
155                 160                 165                 170

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579
Gly Leu Thr Glu Phe Leu Asp Asp Ser His Phe Thr Asn Leu Glu Ser
                175                 180                 185
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627
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ggc aaa tcc agt gaa tac agg cct atg ttt gat gca ata tct aga tgc
675
Gly Lys Ser Ser Glu Tyr Arg Pro Met Phe Asp Ala Ile Ser Arg Cys
        205                 210                 215

ggc gtg atg gta act gaa aga aag aaa act gaa ttt aaa ggg aga gat
723
Gly Val Met Val Thr Glu Arg Lys Lys Thr Glu Phe Lys Gly Arg Asp
    220                 225                 230

ttg gta cag gat ctt ggt agg ctc gtc aag ggt tca gta gaa cct gtt
771
Leu Val Gln Asp Leu Gly Arg Leu Val Lys Gly Ser Val Glu Pro Val
235                 240                 245                 250

cga gat ttg gtc tct ggg ttc gaa tgt gca tca ggc gct ttg ggg tgc
819
Arg Asp Leu Val Ser Gly Phe Glu Cys Ala Ser Gly Ala Leu Gly Cys
                255                 260                 265

ata ctt tct tat gca gaa cta ctt gcg gat gag agc aac tat gga aac
867
Ile Leu Ser Tyr Ala Glu Leu Leu Ala Asp Glu Ser Asn Tyr Gly Asn
            270                 275                 280

tat aca gtc aaa caa tac aac ctc aat agt tac atg aga tta gat tct
915
Tyr Thr Val Lys Gln Tyr Asn Leu Asn Ser Tyr Met Arg Leu Asp Ser
        285                 290                 295

gct gct atg aga gca ctg aat gtt atg gag agc aaa tca gat gct aat
963
Ala Ala Met Arg Ala Leu Asn Val Met Glu Ser Lys Ser Asp Ala Asn
    300                 305                 310

aaa aat ttt agc ttg ttc ggt ctg atg aat aga acg tgt act gct gga
1011
Lys Asn Phe Ser Leu Phe Gly Leu Met Asn Arg Thr Cys Thr Ala Gly
315                 320                 325                 330

atg ggt aaa agg tta ttg cac atg tgg ctg aag caa cct tta cta gat
1059
Met Gly Lys Arg Leu Leu His Met Trp Leu Lys Gln Pro Leu Leu Asp
                335                 340                 345

gta gaa gag att aac tgt agg ctg gat tta gtt caa tca ttc gtg gag
1107
Val Glu Glu Ile Asn Cys Arg Leu Asp Leu Val Gln Ser Phe Val Glu
            350                 355                 360

gat gct gcg ctt cgc caa gat ttg agg cag cat ctg aaa aga att tca
1155
Asp Ala Ala Leu Arg Gln Asp Leu Arg Gln His Leu Lys Arg Ile Ser
        365                 370                 375
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gat att gag cgg ctg aca cac aat ctt gag agg aaa aga gcc agt tta
1203
Asp Ile Glu Arg Leu Thr His Asn Leu Glu Arg Lys Arg Ala Ser Leu
    380                 385                 390

gtg cac gtt gta aaa ctc tat cag tca agt acc aga gta cca tat atc
1251
Val His Val Val Lys Leu Tyr Gln Ser Ser Thr Arg Val Pro Tyr Ile
395                 400                 405                 410

aaa agt gtt ttg gaa cgt cat gat ggg caa ttt gca aca ctc atc agg
1299
Lys Ser Val Leu Glu Arg His Asp Gly Gln Phe Ala Thr Leu Ile Arg
                415                 420                 425

gaa agg tat att gat tct cta gag aaa tgg agt gat gat aat cac ctg
1347
Glu Arg Tyr Ile Asp Ser Leu Glu Lys Trp Ser Asp Asp Asn His Leu
            430                 435                 440

aat aag ttc ata ggt ctt gtg gaa act tct gtt gac ctt gat caa ctt
1395
Asn Lys Phe Ile Gly Leu Val Glu Thr Ser Val Asp Leu Asp Gln Leu
        445                 450                 455

gag aat gga gaa tac atg att tct tct gca tat gac cca aat tta tct
1443
Glu Asn Gly Glu Tyr Met Ile Ser Ser Ala Tyr Asp Pro Asn Leu Ser
    460                 465                 470

gct ctg aag gat gag caa gag aca ttg gag cga caa att cat aat ttg
1491
Ala Leu Lys Asp Glu Gln Glu Thr Leu Glu Arg Gln Ile His Asn Leu
475                 480                 485                 490

cac aaa caa act gcc aat gat ctt gat cta cct att gat aag tca ctt
1539
His Lys Gln Thr Ala Asn Asp Leu Asp Leu Pro Ile Asp Lys Ser Leu
                495                 500                 505

aaa cta gat aaa gaa aca caa ttt gga cac gtc ttc aga att acc aag
1587
Lys Leu Asp Lys Glu Thr Gln Phe Gly His Val Phe Arg Ile Thr Lys
            510                 515                 520

aaa gaa gaa cca aaa gtc agg aag cag cta aat tct cac tac att gtt
1635
Lys Glu Glu Pro Lys Val Arg Lys Gln Leu Asn Ser His Tyr Ile Val
        525                 530                 535

ctc gaa aca cgt aag gat ggg gta aag ttc acc tat aca aaa ctc aaa
1683
Leu Glu Thr Arg Lys Asp Gly Val Lys Phe Thr Tyr Thr Lys Leu Lys
    540                 545                 550

aaa cta gga gat cag ttc cag aag att gta gag gag tac aaa agc tgt
1731
Lys Leu Gly Asp Gln Phe Gln Lys Ile Val Glu Glu Tyr Lys Ser Cys
```

555 560 565 570

cag aaa gaa ttg gta gct cgt gta gtt caa aca gct gcg agt ttc tcc
1779
Gln Lys Glu Leu Val Ala Arg Val Val Gln Thr Ala Ala Ser Phe Ser
575 580 585

gag gtg ttt gca ggt ata gct ggt gta ctt gct gag ttg gat gtg tta
1827
Glu Val Phe Ala Gly Ile Ala Gly Val Leu Ala Glu Leu Asp Val Leu
590 595 600

ctg agt ttt gcg gat ttg gct gcc agt tgc cca act ccc tac aca aga
1875
Leu Ser Phe Ala Asp Leu Ala Ala Ser Cys Pro Thr Pro Tyr Thr Arg
605 610 615

cca aat atc agt cca cca gat aca gga gat att ata ctt gaa ggg tgt
1923
Pro Asn Ile Ser Pro Pro Asp Thr Gly Asp Ile Ile Leu Glu Gly Cys
620 625 630

agg cat cct tgt gtg gaa gct caa gat tgg gtt aac tcc att cct aat
1971
Arg His Pro Cys Val Glu Ala Gln Asp Trp Val Asn Ser Ile Pro Asn
635 640 645 650

gac tgt aga cta gtt agg gga gag agt tgg ttt cag att atc aca ggc
2019
Asp Cys Arg Leu Val Arg Gly Glu Ser Trp Phe Gln Ile Ile Thr Gly
655 660 665

cct aac atg ggt gga aag tcg acc tac att cgg cag gtt ggt gtg aat
2067
Pro Asn Met Gly Gly Lys Ser Thr Tyr Ile Arg Gln Val Gly Val Asn
670 675 680

gtc ctg atg gcc caa gtt ggc tcg ttt gtt cca tgt gac aat gct acc
2115
Val Leu Met Ala Gln Val Gly Ser Phe Val Pro Cys Asp Asn Ala Thr
685 690 695

att tct att cgt gat tgt att ttt gct cgt gtt ggc gct gga gat tgc
2163
Ile Ser Ile Arg Asp Cys Ile Phe Ala Arg Val Gly Ala Gly Asp Cys
700 705 710

cag ctg aga gga gtt tct act ttt atg caa gag atg ctt gag act gca
2211
Gln Leu Arg Gly Val Ser Thr Phe Met Gln Glu Met Leu Glu Thr Ala
715 720 725 730

tcg atc ttg aaa gga gct act gat aga tca ttg att ata att gat gag
2259
Ser Ile Leu Lys Gly Ala Thr Asp Arg Ser Leu Ile Ile Ile Asp Glu
735 740 745

ttg ggc cgt ggg aca tca acc tac gat ggc ttt ggt tta gct tgg gct
2307

```
Leu Gly Arg Gly Thr Ser Thr Tyr Asp Gly Phe Gly Leu Ala Trp Ala
            750                 755                 760

att tgt gag cac att gtt gaa gaa att aaa gca cca aca ttg ttt gcc
2355
Ile Cys Glu His Ile Val Glu Glu Ile Lys Ala Pro Thr Leu Phe Ala
        765                 770                 775

act cac ttt cat gag ctg act gca tta gcc aac aag aat gga gac aat
2403
Thr His Phe His Glu Leu Thr Ala Leu Ala Asn Lys Asn Gly Asp Asn
    780                 785                 790

gga cat aag aaa aat gct ggg ata gca aat ttt cat gtt ttt gca cac
2451
Gly His Lys Lys Asn Ala Gly Ile Ala Asn Phe His Val Phe Ala His
795                 800                 805                 810

att gac cct tct aat cgc aag cta act atg ctt tac aag gtt cac cca
2499
Ile Asp Pro Ser Asn Arg Lys Leu Thr Met Leu Tyr Lys Val His Pro
                815                 820                 825

ggt gct tgt gat cag agt ttt ggt att cat gtt gct gaa ttt gca aat
2547
Gly Ala Cys Asp Gln Ser Phe Gly Ile His Val Ala Glu Phe Ala Asn
            830                 835                 840

ttt cca ccg agt gtt gtg gct ctg gct aga gaa aag gca tct gag ttg
2595
Phe Pro Pro Ser Val Val Ala Leu Ala Arg Glu Lys Ala Ser Glu Leu
        845                 850                 855

gag gat ttc tct cct att gcc ata att cca aat gac att aaa gag gca
2643
Glu Asp Phe Ser Pro Ile Ala Ile Ile Pro Asn Asp Ile Lys Glu Ala
    860                 865                 870

gct tca aaa cgg aag aga gaa ttt gac cgc cat gac gtg tct aga ggt
2691
Ala Ser Lys Arg Lys Arg Glu Phe Asp Arg His Asp Val Ser Arg Gly
875                 880                 885                 890

act gcc aga gct cgg caa ttc tta cag gat ttc gct cag ttg cca ctg
2739
Thr Ala Arg Ala Arg Gln Phe Leu Gln Asp Phe Ala Gln Leu Pro Leu
                895                 900                 905

gat aag atg gat cca aac gtg gtc agg caa aag ttg agc aaa atg aaa
2787
Asp Lys Met Asp Pro Asn Val Val Arg Gln Lys Leu Ser Lys Met Lys
            910                 915                 920

acc gac ctg gag agg gat gca gtt gac tct cac tgg ctt cag caa ttc
2835
Thr Asp Leu Glu Arg Asp Ala Val Asp Ser His Trp Leu Gln Gln Phe
        925                 930                 935

ttt taattcttca gattagaact atcttctatt ctgtgaagct tgggggggaa
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2888
Phe

tgatacttat gggttttgtg gatataactt agcctatctg taaactttca tttaaatcct
2948

taccccaaac atgattctct gtaatcaggg gacttttgta tgcattctgt gttaatagta
3008

agcgttatct tatatggtca aaaaa
3033

<210> 4
<211> 939
<212> PRT
<213> Nicotiana tabacum

<400> 4

Met Asn Glu Asn Leu Glu Glu Gln Ser Lys Leu Pro Glu Leu Lys Leu
1 5 10 15

Asp Ala Lys Gln Ala Gln Gly Phe Leu Ser Phe Phe Lys Thr Leu Pro
20 25 30

Lys Asp Pro Arg Ala Val Arg Leu Phe Asp Arg Arg Asp Tyr Tyr Thr
35 40 45

Ala His Gly Asp Asp Ala Thr Phe Ile Ala Glu Thr Tyr Tyr His Thr
50 55 60

Thr Thr Ala Leu Arg Gln Leu Gly Asn Arg Ala Asp Ala Leu Ser Ser
65 70 75 80

Val Ser Val Ser Arg Asn Met Phe Glu Thr Ile Ala Arg Asp Ile Leu
85 90 95

Leu Glu Arg Met Asp Arg Thr Leu Glu Leu Tyr Glu Gly Ser Gly Ser
100 105 110

Asn Trp Arg Leu Val Lys Ser Gly Thr Pro Gly Asn Leu Gly Ser Phe
115 120 125

Glu Asp Ile Leu Phe Ala Asn Asn Glu Met Gln Asn Ser Pro Val Ile
130 135 140

Ala Ala Leu Ala Pro Asn Phe Gly Gln Asn Gly Cys Glu Val Gly Leu
145 150 155 160

Gly Tyr Val Asp Ile Thr Lys Arg Val Leu Gly Leu Thr Glu Phe Leu
165 170 175

Asp Asp Ser His Phe Thr Asn Leu Glu Ser Ala Leu Val Ala Leu Gly
180 185 190

Cys Arg Glu Cys Leu Val Pro Ala Glu Thr Gly Lys Ser Ser Glu Tyr
195 200 205

Arg Pro Met Phe Asp Ala Ile Ser Arg Cys Gly Val Met Val Thr Glu
210 215 220

Arg Lys Lys Thr Glu Phe Lys Gly Arg Asp Leu Val Gln Asp Leu Gly
225 230 235 240

Arg Leu Val Lys Gly Ser Val Glu Pro Val Arg Asp Leu Val Ser Gly
245 250 255

Phe Glu Cys Ala Ser Gly Ala Leu Gly Cys Ile Leu Ser Tyr Ala Glu
260 265 270

Leu Leu Ala Asp Glu Ser Asn Tyr Gly Asn Tyr Thr Val Lys Gln Tyr
275 280 285

Asn Leu Asn Ser Tyr Met Arg Leu Asp Ser Ala Ala Met Arg Ala Leu
290 295 300

Asn Val Met Glu Ser Lys Ser Asp Ala Asn Lys Asn Phe Ser Leu Phe
305 310 315 320

Gly Leu Met Asn Arg Thr Cys Thr Ala Gly Met Gly Lys Arg Leu Leu
325 330 335

His Met Trp Leu Lys Gln Pro Leu Leu Asp Val Glu Glu Ile Asn Cys
340 345 350

Arg Leu Asp Leu Val Gln Ser Phe Val Glu Asp Ala Ala Leu Arg Gln
355 360 365

Asp Leu Arg Gln His Leu Lys Arg Ile Ser Asp Ile Glu Arg Leu Thr
370 375 380

His Asn Leu Glu Arg Lys Arg Ala Ser Leu Val His Val Val Lys Leu

385 390 395 400

Tyr Gln Ser Ser Thr Arg Val Pro Tyr Ile Lys Ser Val Leu Glu Arg
405 410 415

His Asp Gly Gln Phe Ala Thr Leu Ile Arg Glu Arg Tyr Ile Asp Ser
420 425 430

Leu Glu Lys Trp Ser Asp Asp Asn His Leu Asn Lys Phe Ile Gly Leu
435 440 445

Val Glu Thr Ser Val Asp Leu Asp Gln Leu Glu Asn Gly Glu Tyr Met
450 455 460

Ile Ser Ser Ala Tyr Asp Pro Asn Leu Ser Ala Leu Lys Asp Glu Gln
465 470 475 480

Glu Thr Leu Glu Arg Gln Ile His Asn Leu His Lys Gln Thr Ala Asn
485 490 495

Asp Leu Asp Leu Pro Ile Asp Lys Ser Leu Lys Leu Asp Lys Glu Thr
500 505 510

Gln Phe Gly His Val Phe Arg Ile Thr Lys Lys Glu Glu Pro Lys Val
515 520 525

Arg Lys Gln Leu Asn Ser His Tyr Ile Val Leu Glu Thr Arg Lys Asp
530 535 540

Gly Val Lys Phe Thr Tyr Thr Lys Leu Lys Lys Leu Gly Asp Gln Phe
545 550 555 560

Gln Lys Ile Val Glu Glu Tyr Lys Ser Cys Gln Lys Glu Leu Val Ala
565 570 575

Arg Val Val Gln Thr Ala Ala Ser Phe Ser Glu Val Phe Ala Gly Ile
580 585 590

Ala Gly Val Leu Ala Glu Leu Asp Val Leu Leu Ser Phe Ala Asp Leu
595 600 605

Ala Ala Ser Cys Pro Thr Pro Tyr Thr Arg Pro Asn Ile Ser Pro Pro
610 615 620

Asp Thr Gly Asp Ile Ile Leu Glu Gly Cys Arg His Pro Cys Val Glu
625 630 635 640

Ala Gln Asp Trp Val Asn Ser Ile Pro Asn Asp Cys Arg Leu Val Arg
645 650 655

Gly Glu Ser Trp Phe Gln Ile Ile Thr Gly Pro Asn Met Gly Gly Lys
660 665 670

Ser Thr Tyr Ile Arg Gln Val Gly Val Asn Val Leu Met Ala Gln Val
675 680 685

Gly Ser Phe Val Pro Cys Asp Asn Ala Thr Ile Ser Ile Arg Asp Cys
690 695 700

Ile Phe Ala Arg Val Gly Ala Gly Asp Cys Gln Leu Arg Gly Val Ser
705 710 715 720

Thr Phe Met Gln Glu Met Leu Glu Thr Ala Ser Ile Leu Lys Gly Ala
725 730 735

Thr Asp Arg Ser Leu Ile Ile Ile Asp Glu Leu Gly Arg Gly Thr Ser
740 745 750

Thr Tyr Asp Gly Phe Gly Leu Ala Trp Ala Ile Cys Glu His Ile Val
755 760 765

Glu Glu Ile Lys Ala Pro Thr Leu Phe Ala Thr His Phe His Glu Leu
770 775 780

Thr Ala Leu Ala Asn Lys Asn Gly Asp Asn Gly His Lys Lys Asn Ala
785 790 795 800

Gly Ile Ala Asn Phe His Val Phe Ala His Ile Asp Pro Ser Asn Arg
805 810 815

Lys Leu Thr Met Leu Tyr Lys Val His Pro Gly Ala Cys Asp Gln Ser
820 825 830

Phe Gly Ile His Val Ala Glu Phe Ala Asn Phe Pro Pro Ser Val Val
835 840 845

Ala Leu Ala Arg Glu Lys Ala Ser Glu Leu Glu Asp Phe Ser Pro Ile
850 855 860

Ala Ile Ile Pro Asn Asp Ile Lys Glu Ala Ala Ser Lys Arg Lys Arg
865 870 875 880

Glu Phe Asp Arg His Asp Val Ser Arg Gly Thr Ala Arg Ala Arg Gln
885 890 895

Phe Leu Gln Asp Phe Ala Gln Leu Pro Leu Asp Lys Met Asp Pro Asn
900 905 910

Val Val Arg Gln Lys Leu Ser Lys Met Lys Thr Asp Leu Glu Arg Asp
915 920 925

Ala Val Asp Ser His Trp Leu Gln Gln Phe Phe
930 935

<210> 5
<211> 160
<212> DNA
<213> Nicotiana tabacum

<220>
<221> unsure
<222> (1)..(2)
<223> "n" at positions 1 and 2 can be A, C, G, or T

<400> 5
nnagagaatc ttctctagct ccccgccatt ctctttcccg ccaacccaca tccctccatt
60

ttcccattac tctataaaat cctttgcttt tcatttctac tgcagaaaag ttaaaagaaa
120

aaaaaaaatg aatgaaaatt tggaggaaca gagcaagctt
160

<210> 6
<211> 163
<212> DNA
<213> Nicotiana tabacum

<220>
<221> unsure
<222> (1)..(2)
<223> "n" at positions 1 and 2 can be A, C, G, or T

<220>
<221> unsure
<222> (141)..(141)
<223> "n" at position 141 can be A, C, G, or T

<400> 6
nnaagagaat cttctctagc tccccgccat tctctttccc gccaacccac atccctccat
60

tttcccatta ctctataaaa tcctttgctt ttcatttcta ctgcagaaaa gtttaaagaa
120

aaaaaaaaat gaatgaaaat ntggaggaac agagcaagct tca
163

<210> 7
<211> 163
<212> DNA
<213> Nicotiana tabacum

<220>
<221> unsure
<222> (1)..(2)
<223> "n" at positions 1 and 2 can be A, C, G, or T

<400> 7
nnagagaatc ttctctagct ccccgccatt ctctttcccg ccaacccaca tccctccgtt
60

ttcccattac tctataaaat cctttgcttt tcatttctac tgcagaaaag ttaaaagaaa
120

aaaaaaaaaa tgaatgaaaa tttggaggaa cagagcaagc ttc
163

<210> 8
<211> 165
<212> DNA
<213> Nicotiana tabacum

<220>
<221> unsure
<222> (1)..(2)
<223> "n" at positions 1 and 2 can be A, C, G, or T

<220>
<221> unsure
<222> (161)..(161)
<223> "n" at position 161 can be A, C, G, or T

<400> 8
nnttctctag ctccccgcca ttctctttcc cgccaatcca aatccctcca ttttcctcta
60

ttttcccatt actctataaa atcctttcct tttcatttct acagcataaa ggttaaagaa
120

aaaaaaatga atgaaaattt ggaggaacag agcaagttca ncgaa

165

<210> 9
<211> 166
<212> DNA
<213> Nicotiana tabacum

<220>
<221> unsure
<222> (165)..(166)
<223> "n" at positions 165 abd 166 can be A, C, G, or T

<400> 9
agagaatctt ctctagctcc ccgccattct ctttcccgcc aatccaagtc cctccatttt
60

cctctatttt cccattactc tataaaatcc tttccttttc atttctacag cataaaggtt
120

aaagaaaaaa aaatgaatga aaatttggag gaacagagca agctnn
166

<210> 10
<211> 166
<212> DNA
<213> Nicotiana tabacum

<220>
<221> unsure
<222> (1)..(2)
<223> "n" at positions 1 and 2 can be A, C, G, or T

<400> 10
nnagagaatc ttctctagct ccccgccatt ctctttcccg ccaacccaca tccctccatt
60

ttcccattac tctataaaat cctttgcttt tcatttctac tgcagaaaag ttaaaagaaa
120

aaaaaaaatg aatgaaaatt tggaggaaca gagcaagctt caatcg
166

<210> 11
<211> 166
<212> DNA
<213> Nicotiana tabacum

<220>
<221> unsure
<222> (1)..(2)
<223> "n" at positions 1 and 2 can be A, C, G, or T

<220>

<221> unsure
<222> (157)..(158)
<223> "n" at positions 157 and 158 can be A, C, G, or T

<400> 11
nnagagaatc ttctctagct ccccgccatt ctctttcccg ccaacccaca tccctccatt
60

ttcccattac tctataaaat cctttgcttt tcatttctac tgcagaaaag ttaaaagaaa
120

aaaaaaaatg aatgaaaatt tggaggaaca gagcaanntt caatcg
166

<210> 12
<211> 165
<212> DNA
<213> Nicotiana tabacum

<220>
<221> unsure
<222> (1)..(2)
<223> "n" at positions 1 and 2 can be A, C, G, or T

<400> 12
nnagagaatc ttctctagct ccccgccatt ctctttcccg ccaacccaca tccctccatt
60

ttcccattac tctataaaat cctttgcttt tcatttctac tgcagaaaag ttaaaagaaa
120

aaaaaatgaa tgaaaatttg gaggaacaga gcaagcttca atcga
165

<210> 13
<211> 314
<212> DNA
<213> Nicotiana tabacum

<220>
<221> unsure
<222> (222)..(222)
<223> "n" at position 222 can be A, C, G, or T

<400> 13
gatatcacta gtgattcttt gcaatgaaag ttgcatcatc tccatgagca gtataatagt
60

cccgacgatc aaagaggcga actgccctag ggtccttggg tagggttttg aaaaatgaga
120

gaaatccttg agcttgctta gcatcaagtt taagctcagg aagcttgctc tgttcctcca
180

aaatcgaatt cccgcggccg ccatggcggc cgggagcatg cnacgtcggg cccaattcgc
240

cctatagtga gtcgtattac aattcactgg ccgtcgtttt acaacgtcgt gactgggaaa
300

accctggcgt tacc
314

<210> 14
<211> 314
<212> DNA
<213> Nicotiana tabacum

<400> 14
gatatcacta gtgattcttt gcaatgaaag ttgcatcatc tccatgagca gtataatagt
60

cccgacgatc aaagaggcga actgccctag ggtccttggg cagggttttg aagaatgaga
120

gaaatccttg agcttgctta gcatccagtt taagctcggg aagcttgctc tgttcctcca
180

aaatcgaatt cccgcggccg ccatggcggc cgggagcatg ccgacgtcgg gcccaattcg
240

ccctatagtg agtcgtatta caattcactg gccgtcgttt tacaacgtcg tgactgggaa
300

aaccctggcg ttac
314

<210> 15
<211> 311
<212> DNA
<213> Nicotiana tabacum

<400> 15
atatcactag tgattctttg caatgaaagt tgcatcatct ccatgagatg tataatagtc
60

ccgacgatca aagaggcgaa ctgccctagg gtccttgggc agggttttga agaatgagag
120

aaatccttga gcttgcttag catccagttt aagctcggga agcttgctct gttcctccaa
180

aatcgaattc ccgcggccgc catggcggcc gggagcatgc gacgtcgggc ccaattcgcc
240

ctatagtgag tcgtattaca attcactggc cgtcgtttta caacgtcgtg actgggaaaa
300

ccctggcgtt a
311

<210> 16
<211> 214
<212> DNA
<213> Nicotiana tabacum

<400> 16
gttaaaccct aattcgttaa atgttttatt acattttcag aagtttattc ttacaagtct
60

tttctagctc taatttttta ttatttactt tttctcttca tattatttat tgtgtttaat
120

aaatagaggg ttcatattag ttgttcagct gatttaggga tttaaccgta gtttgattga
180

ttgaaatttg ttaccgtgaa tggttttgtt ttag
214

<210> 17
<211> 223
<212> DNA
<213> Nicotiana tabacum

<400> 17
gtaaaaccct aattctttga atgttttatt acattctcag aagtttattc ttacaagctt
60

ttttctagtt ctaatttttt ttattttata gtttttctct ttatattgtt tactgtgttt
120

aataaatgga tattgatggt tcatattagc ggttcaactg atttggggat ttaactgtag
180

tttgattgat tgatatttgt tattgtgaat ggtcttgttt tag
223

<210> 18
<211> 222
<212> DNA
<213> Nicotiana tabacum

<400> 18
gtaaaaccct aattctttga atgttttatt acattctcag aagtttattc ttacaagctt
60

ttttctagtt ctaatttttt ttattttata gtttttctct ttatattgtt tactgtgttt
120

aataaatgga tattgatggt tcatattagc ggttcaactg atttggggat ttaactgtag
180

tttgattgat gatatttgtt attgtgaatg gttttgtttt ag
222

<210> 19

<211> 107
<212> DNA
<213> Nicotiana tabacum

<400> 19
gtaacttttt catattattc attctgttta aatagttatt gcaccttcac ttgtagagaa
60

aattgctcgg cggttcactt aatagagaac ttttgatttt tttgcag
107

<210> 20
<211> 105
<212> DNA
<213> Nicotiana tabacum

<400> 20
gtaacttttt catattattc attctgttta aatagttatt gcaccttcac ttgtagagaa
60

aattgttagt cgggttgctt aatagagaac tctttttttt tgcag
105

<210> 21
<211> 106
<212> DNA
<213> Nicotiana tabacum

<220>
<221> unsure
<222> (11)..(16)
<223> "n" at positions 11-16 can be A, C, G, or T

<400> 21
gtaaactttt nnnnnnattc attctgttca aacggttatt gcaccttcac ttgtagagaa
60

aattgttagt cggtttgctt aatagagaac tctttttttt ttgcag
106

<210> 22
<211> 5
<212> PRT
<213> MutS consensus sequence

<400> 22

Thr Gly Pro Asn Met
1 5

<210> 23
<211> 5
<212> PRT
<213> MutS consensus sequence

<400> 23

Phe Ala Thr His Tyr
1 5

<210> 24
<211> 20
<212> DNA
<213> oligonucleotide primer

<400> 24
gtaacagggc ctaacatggg
20

<210> 25
<211> 19
<212> DNA
<213> oligonucleotide primer

<400> 25
ggaagtgagt agcaaacag
19

<210> 26
<211> 19
<212> DNA
<213> oligonucleotide primer

<400> 26
caggccctaa catgggtgg
19

<210> 27
<211> 20
<212> DNA
<213> oligonucleotide primer

<400> 27
aatgaaatgc aagattctcc
20

<210> 28
<211> 20
<212> DNA
<213> oligonucleotide primer

<400> 28
gaagcttgct ctgttcctcc
20

<210> 29
<211> 17
<212> DNA
<213> oligonucleotide primer

<220>
<221> misc_feature
<222> (3)..(3)
<223> "n" at position 3 can be A, C, G, or T

<220>
<221> misc_feature
<222> (6)..(6)
<223> "n" at position 6 can be A, C, G, or T

<220>
<221> misc_feature
<222> (9)..(9)
<223> "n" at position 9 can be A, C, G, or T

<400> 29
acnggnccna ayatggg
17

<210> 30
<211> 17
<212> DNA
<213> oligonucleotide primer

<220>
<221> misc_feature
<222> (9)..(9)
<223> "n" at position 9 can be A, C, G, or T

<220>
<221> misc_feature
<222> (12)..(12)
<223> "n" at position 12 can be A, C, G, or T

<400> 30
tgyaartgng tncgraa
17

<210> 31
<211> 19
<212> DNA
<213> oligonucleotide primer

<400> 31
caggccctaa catgggtgg
19

<210> 32
<211> 6
<212> PRT

<213> MSH2 consensus sequence

<400> 32

Asp Tyr Tyr Thr Ala His
1 5

<210> 33
<211> 20
<212> DNA
<213> oligonucleotide primer

<400> 33
gattattata cagctcatgg
20

<210> 34
<211> 6
<212> PRT
<213> MSH2 consensus sequence

<400> 34

Met Trp Leu Lys Gln Pro
1 5

<210> 35
<211> 17
<212> DNA
<213> oligonucleotide primer

<400> 35
atgtggctga aacaacc
17

<210> 36
<211> 22
<212> DNA
<213> oligonucleotide primer

<400> 36
cttatgtcca ttgtctccat tc
22

<210> 37
<211> 20
<212> DNA
<213> oligonucleotide primer

<400> 37
gtccattgtc tccattcttg
20

<210> 38
<211> 20

<212> DNA
<213> oligonucleotide primer

<400> 38
gcaccccaaa gcgcctgatg
20

<210> 39
<211> 23
<212> DNA
<213> oligonucleotide primer

<400> 39
ctgatgcaca ttcgaaccca gag
23

<210> 40
<211> 22
<212> DNA
<213> oligonucleotide primer

<400> 40
acatatagtt caagagtacg gt
22

<210> 41
<211> 22
<212> DNA
<213> oligonucleotide primer

<400> 41
gctattgttt caaacatgtt tc
22

<210> 42
<211> 22
<212> DNA
<213> oligonucleotide primer

<400> 42
ttggaggaac agagcaagct tc
22